

0570
1211

#8

OIPE

RAW SEQUENCE LISTING

DATE: 12/12/2001

PATENT APPLICATION: US/09/881,457A

TIME: 11:41:39

Input Set : A:\09881457.txt

Output Set: N:\CRF3\12112001\I881457A.raw

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3 <110> APPLICANT: Cochran, Mark D
4     Cook, Stephanie M
5     Wild, Martha A
7 <120> TITLE OF INVENTION: Novel Avian Herpes Virus and Uses Thereof
9 <130> FILE REFERENCE: SY01105K1QKQK
11 <140> CURRENT APPLICATION NUMBER: US 09/881,457A
12 <141> CURRENT FILING DATE: 2001-06-14
14 <150> PRIOR APPLICATION NUMBER: 09/426,352
15 <151> PRIOR FILING DATE: 1999-10-25
17 <150> PRIOR APPLICATION NUMBER: 08/804,372
18 <151> PRIOR FILING DATE: 1997-02-21
20 <150> PRIOR APPLICATION NUMBER: PCT/US95/10245
21 <151> PRIOR FILING DATE: 1995-08-09
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24 <151> PRIOR FILING DATE: 1996-06-13
26 <150> PRIOR APPLICATION NUMBER: 08/288,065
27 <151> PRIOR FILING DATE: 1994-08-09
29 <150> PRIOR APPLICATION NUMBER: PCT/US93/05681
30 <151> PRIOR FILING DATE: 1993-06-14
32 <150> PRIOR APPLICATION NUMBER: 08/023,610
33 <151> PRIOR FILING DATE: 1993-02-26
35 <150> PRIOR APPLICATION NUMBER: 07/898,087
36 <151> PRIOR FILING DATE: 1992-06-12
38 <160> NUMBER OF SEQ ID NOS: 5
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43 <211> LENGTH: 3570
44 <212> TYPE: DNA
45 <213> ORGANISM: Newcastle disease virus
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49 <222> LOCATION: (1194)..(2888)
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54 <222> LOCATION: (1355)
55 <223> OTHER INFORMATION: n = any nucleotide
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62 ttatcgccg atagagatgg cgatattgga aaaatcgata ttgaaaata tggcatattg 180
64 aaaatgtcgc cgatgtgagt ttctgtgtaa ctgatattctg gcgatagcgc ttatatcggt 240
66 tacgggggat ggcatagac gactttggcg acttgggcga ttctgtgtgt cgcaaataatc 300
68 gcagtttcga tataggtgac agacgatatg aggctatatc gccgatagag gcgacatcaa 360
70 gctggcacat ggccaatgca tatcgatcta tacattgaat caatattggc aattagccat 420
72 attagtcatt gggtatatag cataaatcaa tattggctat tggccattgc atacgttgta 480
74 tctatatcat aatatgtaca ttatatattgg ctcatgtcca atatgaccgc catgttgaca 540

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80 ccccgccca ttgacgtcaa taatgacgta tgttcccata gtaacgcaa tagggacttt 720
82 ccattgacgt caatgggtgg agtatattacg gtaaactgcc cacttggcag tacatcaagt 780
84 gtatcatatg ccaagtccgc cccctattga cgtcaatgac ggtaaattggc cgcctggca 840
86 ttatgccag tacatgacct tacgggactt tcctacttgg cagtacatct acgtattagt 900
88 catcgctatt accatggtga tgcggttttg gcagtacacc aatgggcgtg gatagcggtt 960
90 tgactcacgg ggatttccaa gtctccaccc cattgacgtc aatgggagtt tgttttggca 1020
92 ccaaatcaa cgggactttc caaatgtcg taataacccc gcccggttga cgcaaatggg 1080
94 cggtaggcgt gtacggtggg aggtctatat aagcagagct cgtttagtga accgtcagat 1140
96 cgcctggaga cgccatccac gctgttttga cctccataga agacaccggg acc atg 1196
97 Met
98 1
100 gat cga tcc cgg ttg gcg ccc tcc agg tgc agg atg ggc tcc aga cct 1244
101 Asp Arg Ser Arg Leu Ala Pro Ser Arg Cys Arg Met Gly Ser Arg Pro
102 5 10 15
104 tct acc aag aac cca gca cct atg atg ctg act atc cgg gtc gcg ctg 1292
105 Ser Thr Lys Asn Pro Ala Pro Met Met Leu Thr Ile Arg Val Ala Leu
106 20 25 30
108 gta ctg agt tgc atc tgt ccg gca aac tcc att gat ggc agg cct ctt 1340
109 Val Leu Ser Cys Ile Cys Pro Ala Asn Ser Ile Asp Gly Arg Pro Leu
110 35 40 45
W--> 112 gca gct gca gga ctn tgg tta cag gag aca aag caa tca aca tat aca 1388
W--> 113 Ala Ala Ala Gly Xaa Trp Leu Gln Glu Thr Lys Gln Ser Thr Tyr Thr
114 50 55 60 65
116 cct cat ccc aga cag gtc aat cat att aag ctc ctc ccg aat ctg cca 1436
117 Pro His Pro Arg Gln Val Asn His Ile Lys Leu Leu Pro Asn Leu Pro
118 70 75 80
120 aag gat aag gag gca tgt gcg aaa gcc ccc ttg gat gca tac aac agg 1484
121 Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro Leu Asp Ala Tyr Asn Arg
122 85 90 95
124 aca ttg acc act ttg ctc acc ccc ctt ggt gac tct atc cgt agg ata 1532
125 Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly Asp Ser Ile Arg Arg Ile
126 100 105 110
128 caa gag tct gtg act aca tct gga ggg ggg aga cag ggg cgc ctt ata 1580
129 Gln Glu Ser Val Thr Thr Ser Gly Gly Gly Arg Gln Gly Arg Leu Ile
130 115 120 125
132 ggc gcc att att ggc ggt gtg gct ctt ggg gtt gca act gcc gca caa 1628
133 Gly Ala Ile Ile Gly Gly Val Ala Leu Gly Val Ala Thr Ala Ala Gln
134 130 135 140 145
136 ata aca gcg gcc gca gct ctg ata caa gcc aaa caa aat gct gcc aac 1676
137 Ile Thr Ala Ala Ala Ala Leu Ile Gln Ala Lys Gln Asn Ala Ala Asn
138 150 155 160
140 atc ctc cga ctt aaa gag agc att gcc gca acc aat gag gct gtg cat 1724
141 Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala Thr Asn Glu Ala Val His
142 165 170 175
144 gag gtc act gac gga tta tcg caa cta gca gtg gca gtt ggg aag atg 1772
145 Glu Val Thr Asp Gly Leu Ser Gln Leu Ala Val Ala Val Gly Lys Met
146 180 185 190

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150		195					200					205					
152	tgc	atc	aaa	att	gca	cag	caa	gtt	ggt	gta	gag	ctc	aac	ctg	tac	cta	1868
153	Cys	Ile	Lys	Ile	Ala	Gln	Gln	Val	Gly	Val	Glu	Leu	Asn	Leu	Tyr	Leu	
154	210					215					220					225	
156	acc	gaa	tcg	act	aca	gta	ttc	gga	cca	caa	atc	act	tca	cct	gcc	tta	1916
157	Thr	Glu	Ser	Thr	Thr	Val	Phe	Gly	Pro	Gln	Ile	Thr	Ser	Pro	Ala	Leu	
158					230					235					240		
160	aac	aag	ctg	act	att	cag	gca	ctt	tac	aat	cta	gct	ggt	ggg	aat	atg	1964
161	Asn	Lys	Leu	Thr	Ile	Gln	Ala	Leu	Tyr	Asn	Leu	Ala	Gly	Gly	Asn	Met	
162				245						250					255		
164	gat	tac	tta	ttg	act	aag	tta	ggt	ata	ggg	aac	aat	caa	ctc	agc	tca	2012
165	Asp	Tyr	Leu	Leu	Thr	Lys	Leu	Gly	Ile	Gly	Asn	Asn	Gln	Leu	Ser	Ser	
166			260					265					270				
168	tta	atc	ggt	agc	ggc	tta	atc	acc	ggt	aac	cct	att	cta	tac	gac	tca	2060
169	Leu	Ile	Gly	Ser	Gly	Leu	Ile	Thr	Gly	Asn	Pro	Ile	Leu	Tyr	Asp	Ser	
170		275					280						285				
172	cag	act	caa	ctc	ttg	ggt	ata	cag	gta	act	cta	cct	tca	gtc	ggg	aac	2108
173	Gln	Thr	Gln	Leu	Leu	Gly	Ile	Gln	Val	Thr	Leu	Pro	Ser	Val	Gly	Asn	
174	290					295					300					305	
176	cta	aat	aat	atg	cgt	gcc	acc	tac	ttg	gaa	acc	tta	tcc	gta	agc	aca	2156
177	Leu	Asn	Asn	Met	Arg	Ala	Thr	Tyr	Leu	Glu	Thr	Leu	Ser	Val	Ser	Thr	
178					310					315					320		
180	acc	agg	gga	ttt	gcc	tcg	gca	ctt	gtc	cca	aaa	gtg	gtg	aca	cgg	gtc	2204
181	Thr	Arg	Gly	Phe	Ala	Ser	Ala	Leu	Val	Pro	Lys	Val	Val	Thr	Arg	Val	
182				325						330					335		
184	ggt	tct	gtg	ata	gaa	gaa	ctt	gac	acc	tca	tac	tgt	ata	gaa	act	gac	2252
185	Gly	Ser	Val	Ile	Glu	Glu	Leu	Asp	Thr	Ser	Tyr	Cys	Ile	Glu	Thr	Asp	
186			340					345					350				
188	tta	gat	tta	tat	tgt	aca	aga	ata	gta	acg	ttc	cct	atg	tcc	cct	ggt	2300
189	Leu	Asp	Leu	Tyr	Cys	Thr	Arg	Ile	Val	Thr	Phe	Pro	Met	Ser	Pro	Gly	
190		355					360					365					
192	att	tac	tcc	tgc	ttg	agc	ggc	aat	aca	tcg	gcc	tgt	atg	tac	tca	aag	2348
193	Ile	Tyr	Ser	Cys	Leu	Ser	Gly	Asn	Thr	Ser	Ala	Cys	Met	Tyr	Ser	Lys	
194	370					375					380					385	
196	acc	gaa	ggc	gca	ctt	act	aca	cca	tat	atg	act	atc	aaa	ggc	tca	gtc	2396
197	Thr	Glu	Gly	Ala	Leu	Thr	Thr	Pro	Tyr	Met	Thr	Ile	Lys	Gly	Ser	Val	
198					390					395					400		
200	atc	gct	aac	tgc	aag	atg	aca	aca	tgt	aga	tgt	gta	aac	ccc	ccg	ggt	2444
201	Ile	Ala	Asn	Cys	Lys	Met	Thr	Thr	Cys	Arg	Cys	Val	Asn	Pro	Pro	Gly	
202				405						410					415		
204	atc	ata	tcg	caa	aac	tat	gga	gaa	gcc	gtg	tct	cta	ata	gat	aaa	caa	2492
205	Ile	Ile	Ser	Gln	Asn	Tyr	Gly	Glu	Ala	Val	Ser	Leu	Ile	Asp	Lys	Gln	
206			420					425					430				
208	tca	tgc	aat	gtt	tta	tcc	tta	ggc	ggg	ata	act	tta	agg	ctc	agt	ggg	2540
209	Ser	Cys	Asn	Val	Leu	Ser	Leu	Gly	Gly	Ile	Thr	Leu	Arg	Leu	Ser	Gly	
210		435					440					445					
212	gaa	ttc	gat	gta	act	tat	cag	aag	aat	atc	tca	ata	caa	gat	tct	caa	2588

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217 Val Ile Ile Thr Gly Asn Leu Asp Ile Ser Thr Glu Leu Gly Asn Val
218                               470                               475                               480
220 aac aac tcg atc agt aat gcc ttg aat aag tta gag gaa agc aac aga 2684
221 Asn Asn Ser Ile Ser Asn Ala Leu Asn Lys Leu Glu Glu Ser Asn Arg
222                               485                               490                               495
224 aaa cta gac aaa gtc aat gtc aaa ctg acc agc aca tct gct ctc att 2732
225 Lys Leu Asp Lys Val Asn Val Lys Leu Thr Ser Thr Ser Ala Leu Ile
226                               500                               505                               510
228 acc tat atc gtt ttg act atc ata tct ctt gtt ttt ggt ata ctt agc 2780
229 Thr Tyr Ile Val Leu Thr Ile Ile Ser Leu Val Phe Gly Ile Leu Ser
230                               515                               520                               525
232 ctg att cta gca tgc tac cta atg tac aag caa aag gcg caa caa aag 2828
233 Leu Ile Leu Ala Cys Tyr Leu Met Tyr Lys Gln Lys Ala Gln Gln Lys
234 530                               535                               540                               545
236 acc tta tta tgg ctt ggg aat aat acc cta gat cag atg aga gcc act 2876
237 Thr Leu Leu Trp Leu Gly Asn Asn Thr Leu Asp Gln Met Arg Ala Thr
238                               550                               555                               560
240 aca aaa atg tga acacagatga ggaacgaagg ttccctaata agtaatttgt 2928
241 Thr Lys Met
244 gtgaaagtgc tggtagtctg tcagttcgga gagttaagaa aaaaaaaaaa cccccccccc 2988
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252 actctgtoga taccacaccg agacccatt gggaccaata cgcgcgctt tcttcctttt 3228
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262 cacgaacacc gggcgctctgt ggctgcaaaa caccgccgac ccccaaaaac caccgcgcgg 3528
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272 <220> FEATURE:
273 <221> NAME/KEY: misc_feature
274 <222> LOCATION: (54)
275 <223> OTHER INFORMATION: Xaa = any amino acid
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282 20 25 30
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285 35 40 45
W--> 287 Leu Ala Ala Ala Gly Xaa Trp Leu Gln Glu Thr Lys Gln Ser Thr Tyr

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291 65      70      75      80
293 Pro Lys Asp Lys Glu Ala Cys Ala Lys Ala Pro Leu Asp Ala Tyr Asn
294      85      90      95
296 Arg Thr Leu Thr Thr Leu Leu Thr Pro Leu Gly Asp Ser Ile Arg Arg
297      100      105      110
299 Ile Gln Glu Ser Val Thr Thr Ser Gly Gly Gly Arg Gln Gly Arg Leu
300      115      120      125
302 Ile Gly Ala Ile Ile Gly Gly Val Ala Leu Gly Val Ala Thr Ala Ala
303      130      135      140
305 Gln Ile Thr Ala Ala Ala Leu Ile Gln Ala Lys Gln Asn Ala Ala
306 145      150      155      160
308 Asn Ile Leu Arg Leu Lys Glu Ser Ile Ala Ala Thr Asn Glu Ala Val
309      165      170      175
311 His Glu Val Thr Asp Gly Leu Ser Gln Leu Ala Val Ala Val Gly Lys
312      180      185      190
314 Met Gln Gln Phe Val Asn Asp Gln Phe Asn Lys Thr Ala Gln Glu Leu
315      195      200      205
317 Asp Cys Ile Lys Ile Ala Gln Gln Val Gly Val Glu Leu Asn Leu Tyr
318      210      215      220
320 Leu Thr Glu Ser Thr Thr Val Phe Gly Pro Gln Ile Thr Ser Pro Ala
321 225      230      235      240
323 Leu Asn Lys Leu Thr Ile Gln Ala Leu Tyr Asn Leu Ala Gly Gly Asn
324      245      250      255
326 Met Asp Tyr Leu Leu Thr Lys Leu Gly Ile Gly Asn Asn Gln Leu Ser
327      260      265      270
329 Ser Leu Ile Gly Ser Gly Leu Ile Thr Gly Asn Pro Ile Leu Tyr Asp
330      275      280      285
332 Ser Gln Thr Gln Leu Leu Gly Ile Gln Val Thr Leu Pro Ser Val Gly
333      290      295      300
335 Asn Leu Asn Asn Met Arg Ala Thr Tyr Leu Glu Thr Leu Ser Val Ser
336 305      310      315      320
338 Thr Thr Arg Gly Phe Ala Ser Ala Leu Val Pro Lys Val Val Thr Arg
339      325      330      335
341 Val Gly Ser Val Ile Glu Glu Leu Asp Thr Ser Tyr Cys Ile Glu Thr
342      340      345      350
344 Asp Leu Asp Leu Tyr Cys Thr Arg Ile Val Thr Phe Pro Met Ser Pro
345      355      360      365
347 Gly Ile Tyr Ser Cys Leu Ser Gly Asn Thr Ser Ala Cys Met Tyr Ser
348      370      375      380
350 Lys Thr Glu Gly Ala Leu Thr Thr Pro Tyr Met Thr Ile Lys Gly Ser
351 385      390      395      400
353 Val Ile Ala Asn Cys Lys Met Thr Thr Cys Arg Cys Val Asn Pro Pro
354      405      410      415
356 Gly Ile Ile Ser Gln Asn Tyr Gly Glu Ala Val Ser Leu Ile Asp Lys
357      420      425      430
359 Gln Ser Cys Asn Val Leu Ser Leu Gly Gly Ile Thr Leu Arg Leu Ser
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VERIFICATION SUMMARY

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